

**Amendments to the claims:**

Please amend the claims as shown below.

1. (Currently Amended) A composition comprising a substantially purified Avilll peptide polypeptide with cellulase activity and having at least 90 99% identity to SEQ ID NO. 1, ~~said Avilll peptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74\_Ace) enzyme and a carbohydrate binding domain (CBD) III.~~
2. (Currently Amended) The composition of claim 1 wherein the ~~polypeptide Avilll peptide is further defined as comprising comprises a glycosyl hydrolase family 74 (GH74\_Ace) enzyme, a carbohydrate binding domain (CBD) III, a linker, and a signal sequence.~~
3. (Cancelled)
4. (Currently Amended) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the ~~polypeptide Avilll peptide~~ is further defined as comprising a length of about 80 to about 150 amino acids.
5. (Currently Amended) The composition of claim 1 or 2 wherein the carbohydrate binding domain (CBD) III of the ~~polypeptide Avilll peptide~~ is further defined as comprising a length of about 90 amino acids.
6. (Currently Amended) The composition of claim 1 or 2 wherein the glycosyl hydrolase family 74 enzyme catalytic domain is further defined as including a polypeptide of sequence identical to SEQ ID NO: 3.

7. (Currently Amended) The composition of claim 4 2 wherein the carbohydrate binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 4.

8. (Currently Amended) The composition of claim 4 2 wherein the carbohydrate-binding domain (CBD) III is further defined as comprising the polypeptide sequence of SEQ ID NO: 5.

9. (Currently Amended) The composition of claim 4 2 wherein said polypeptide Avilll protein comprises sequences identical to the polypeptides of SEQ ID NO: 3 and SEQ ID NO: 4.

10-11. (Cancelled)

12. (Currently Amended) An isolated A purified polypeptide Avilll peptide having at least 99% identity to a polypeptide sequence of SEQ ID NO: 1.

13. (Cancelled)

14. (Currently Amended) An industrial mixture suitable for degrading cellulose, such mixture comprising the Avilll polypeptide of claim 1.

15. (Previously presented) The industrial mixture of claim 14 further defined as comprising a detergent.

16-27 (Cancelled)

28. (Currently Amended) An isolated A purified polypeptide having at least 99% identity to molecule comprising at least one a polypeptide sequence selected from the group consisting of:

- a) a polypeptide sequence of SEQ ID NO: 3;
- b) a polypeptide sequence of SEQ ID NO: 4;

- c) a polypeptide sequence of SEQ ID NO: 5; and
- d) a polypeptide sequence of SEQ ID NO: 1; and
- e) combinations thereof.

29. (Cancelled)

30. (Original) A fusion protein comprising the polypeptide of claim 28 and a heterologous peptide.

31. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a substrate targeting moiety.

32. (Original) The fusion protein of claim 30, wherein the heterologous peptide is a peptide tag.

33. (Previously presented) The fusion protein of claim 32, wherein the peptide tag is 6-His, thioredoxin, hemagglutinin, glutathione S-transferase, or OmpA signal sequence tag.

34. (Original) The fusion protein of claim 30, wherein the heterologous peptide is an agent that promotes polypeptide oligomerization.

35. (Original) The fusion protein of claim 34, wherein the agent is a leucine zipper.

36. (Currently Amended) A cellulase-substrate complex comprising the isolated polypeptide molecule of claim 28 bound to cellulose.

37-42 (Cancelled)

43. (Currently Amended) A composition comprising the polypeptide molecule of claim 28 and a carrier.

44-46. (Cancelled)

47. (Currently Amended) The composition of claim 1 wherein said catalytic domain of GH74\_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (\*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AvIII\_Aac):

|                       |   |
|-----------------------|---|
| GH74_Ace<br>AvIII_Aac | ATTQPYTWSNVAIGGGG-FVDGIVFNEGAPGILYVRTDIGGMYRWDAANGRWIPLLDWVG<br>AASQAYTWKNVTGGGGFTPGIVFNPSAKGVAYARTDIGGAYRLNSDD-TWTPLMDWVG<br>*:.*.***.*. *** * .***** .* : *.*.***** * : : * *;****                |
| GH74_Ace<br>AvIII_Aac | WNNWGYNGVVSIAADPINTNKVWAAGVGMYTNSWDPNDGAILRSSDQGATWQITPLPFKLG<br>NDTWHWDWGIDALATDPVTDDRVYAVGMYTNEWDPNVGSILRSTDQGDTWTETKLPFKVG<br>.** * : :*;*:;*:;*.*****;**** *;*****;*** ** * ****;*              |
| GH74_Ace<br>AvIII_Aac | GNMPGRGMGERLAVIDPNNDNILYFGAPSGKGLWRSTDSGATWSQMTNFPDVGTYIANPTD<br>GNMPGRGMGERLAVIDPNKNSILYFGARSGHGLWKSTDYGATWSNVTSTWTGTYFQDSSS<br>*****;*****;*****;*****;*****;*****;*****;*****;*****;*****;*****; |
| GH74_Ace<br>AvIII_Aac | TTGYQSDIQGVVVWAFDKSSSLGQASKTIFVGVADPNNPVFWSRDGATWQAVPGAP-T<br>T-T-YTSDPVGIAWTFDSTSOGSSATPRIFVGVADAGKSVFKSEDAGATWAWVSGEPOY<br>* * ** * :*.**;*.**;*.**;*.**; * *****.:.** * .*.**** * .*,* *         |
| GH74_Ace<br>AvIII_Aac | GFIPHKGVFDPVNHVLYIATSNTGGPYDGSSGDVWKFSVTSGTWTRISPVPSTDANDYF<br>GFLPHKGVLSPEEKTLYISYANGAGPYDGTVHKYNITSGVWTDISP---TSLASTYY<br>**;*****;* :.***; * .*****;* * * :.***;***.** *** * .*. * :             |
| GH74_Ace<br>AvIII_Aac | GYSGLTIDRQHPNTIMVATQISWWPDTIIFRSTDGGATWTRIWDTSPNRSRLRYVLDIS<br>GYGGLSVDLQVPGTLMVAALNCWWPDELIFRSTDGGATWSPIEWNGGPSINYYYSYDIS<br>**.**;* * .*,*;***; * .***** ;*****;*****; * :*..**. . * ***          |
| GH74_Ace<br>AvIII_Aac | AEPWLTFGVQPNNPPVSPKLGWMDEAMAIDPFNSDRMLYGTGATLYATNDLTKWDSSGGQI<br>NAPWIQDTTSTDQFP--VRVGWMVEALAIDPFDSNHLYGTGLTVYGGHDLTNWDSKHNV<br>**; . . . : :*** *;*****;*: * .***** *.*. : ***;*** . :             |
| GH74_Ace<br>AvIII_Aac | HIAPMVKGLEETAVNDLISPPSGAPLISALGDLGGFTHADVTAVPSTIFTSPVFTTGTGV<br>TVKSLAVGIEEMAVGLITPPGGPALLSAVGDDGGFYHSSDLAAAPNQAYHTPTYGTNGI<br>. . . *;** * * .**;**.**.*;**;** * * *; *.*. : :*. * . .             |
| GH74_Ace<br>AvIII_Aac | DYAELNPSIIVRAGSFDPSSQPNDRHVAFSTDGGKNWFQGSEPGVTTGGTVAASADGSR<br>DYAGNKPSNIVRSGASDDYP----TLALSSNFGSTWYADYAATSTGTGAVALSADGDT<br>*** ;** ***;*: * . : *;*:; * .. * : . . * *;*** ****.                  |
| GH74_Ace<br>AvIII_Aac | FVWAPGDPGPVYYAVGFGNSWAASQGPANAQIRSDRVNPKTFYALSNGTFYRSTDGGV<br>VLLMSSTSGALVSKSQG---TLAVSSLPSGAVIASDKSDNTVYGGSAGAIYVSKNTAT<br>. . . . * * : * . : * .. :*;. * *; : . . *. * *;* * : ..                |
| GH74_Ace<br>AvIII_Aac | TFQPVAAGLPSSGAVGVMFHAVPGKEGDLWLAASSGLYHSTNGSSWSAI-TGVSSAVNV<br>SFTKTVS-LGSSTTVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTFTQIGSGVTAGWSF<br>*: . . * * *;*. * . * *;*: * . : . . *;*: * . : * : * : ..           |
| GH74_Ace<br>AvIII_Aac | GFGKSAPGSSYPAVFVVGTIGGVTGAYRSDDCGTTWVLINDDHQYGN-WGQAITGDHAN<br>GFGKASSTGCSYVIYGFITDGAAGLFKSEDAGTNWQVISDASHGFGSGSANVVNGDLQT<br>****;*.** .: . * .;* : * : *;*.**.** : * . * : * . . . .** .          |
| GH74_Ace<br>AvIII_Aac | LRRVYIGTNGRGRIVYGDIGGAPSG<br>YGRVFRGHRERPGHLLRQSQREPAG<br>**; * : * : : * : .   |

48. (Currently Amended) The composition of claim 47 wherein said Avill peptide polypeptide retains at least the same level of cellulase activity and thermal tolerability as those exhibited by the peptide of SEQ ID NO. 1.

49. (Currently Amended) A composition comprising a substantially purified AvI<sub>III</sub> peptide polypeptide having at least 99-95% identity to SEQ ID NO. 1, said AvI<sub>III</sub> peptide polypeptide comprising a catalytic domain of a glycosyl hydrolase family 74 (GH74\_Ace) enzyme and a carbohydrate binding domain (CBD) III.

50. (Currently Amended) The composition of claim 49 wherein said catalytic domain of GH74\_Ace having a sequence identical to SEQ ID NO. 3 in each conserved position marked by an asterisk (\*), as shown below in comparison to *Aspergillus aculeatus* Avicelase III (AvIII\_Aac):

\*\*\* :\*\* \*\*\*;\*: \* . . . :\*;\*: \* . . . \* \*;\* \*\*\*\*.

|                        |  |
|------------------------|--|
| GH74_Ace<br>AviIII_Aac | FVWAPGDPGPVYAVGFGNSWAASQGVPAQIRSDRVNPKTFYALSNGTFYRSTDGGV<br>VLLMSSTSGALVSKSQG---TLTAVSSLPSGAVIASDKSDNTVFYGGSAGAIYVSKNTAT<br>. . . . . * * ; * : * . . :* . . :* . * * ; : . . * . * * ; * . .    |
| GH74_Ace<br>AviIII_Aac | TFQPVAAGLPSSGAVGVMFHAVPGKEGDLWLAASSGLYHSTNGSSWSAI-TGVSSAVNV<br>SFTKTVS-LGSSTTVNAIR-AHPSIAGDVWASTDKGLWHSTDYGSTFTQIGSGVTAGWSF<br>. * . . . * * ; * . . : * . * . * ; * : . . * ; * ; * . * ; * . . |
| GH74_Ace<br>AviIII_Aac | GFGKSAPGSSYPAVFVVGTIGGVTGAYRSDDCGTTWVLINDDHQYGN-WGQAITGDHAN<br>GFGKASSTGSYVVIYGFFTIDGAAGLFKSEDAGTNWQVISDASHFGSGSANVVNGDLQT<br>*****; . . * . . : . . * . . ; * . : * . * . * . * . . . . * .     |
| GH74_Ace<br>AviIII_Aac | LRRVYIGTNGRIVYGDIGGAPSG<br>YGRVFRGHERPGHLLRQSREPAG<br>***: * : * : : : * ; *   |

51. (Currently Amended) The composition of claim 50 wherein said AviIII peptide polypeptide retains at least the same level of cellulase activity and thermal tolerability as those exhibited by the peptide of SEQ ID NO. 1.

52. (Currently Amended) A composition comprising a substantially purified AviIII peptide polypeptide having an amino acid sequence identical to SEQ ID NO. 1, said AviIII peptide polypeptide comprising characterized by a catalytic domain of a glycosyl hydrolase family 74 (GH74\_Ace) enzyme and a carbohydrate binding domain (CBD) III.

53. (Currently Amended) A composition comprising a substantially purified AviIII peptide polypeptide, said AviIII peptide polypeptide comprising characterized by a catalytic domain of a glycosyl hydrolase family 74 (GH74\_Ace) enzyme and a carbohydrate binding domain (CBD) III, said catalytic domain of GH74\_Ace having a sequence that is at least 90 99% identical to SEQ ID NO. 3.

54. (Currently Amended) The composition of claim 51 wherein said catalytic domain of GH74\_Ace has a sequence identical to SEQ ID NO. 3.

55. (New) A composition comprising a genetically engineered polypeptide expressed in a heterologous host cell, said polypeptide having at least 99% identity to SEQ ID NO. 1.

56. (New) A composition comprising a genetically engineered polypeptide expressed in a heterologous host cell, said polypeptide comprising a sequence having at least 99% identity to SEQ ID NO. 3.